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RAW SEQUENCE LISTING DATE: 12/07/2001 PATENT APPLICATION: US/09/961,201 TIME: 12:18:52

Input Set : N:\Crf3\RULE60\09961201.txt
Output Set: N:\CRF3\12072001\1961201.raw

## SEQUENCE LISTING

```
3 (1) GENERAL INFORMATION:
             (i) APPLICANT: DIXIT, VISHVA M.
     5
                            HE, WEI-WU
     6
                            KIKLY, KRISTINE K.
     7
                            RUBEN, STEVEN M.
     8
            (ii) TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING
    10
                                     ENZYME LIKE APOPTOTIC PROTEASE-6
    11
           (iii) NUMBER OF SEQUENCES: 11
    13
            (iv) CORRESPONDENCE ADDRESS:
     15
                  (A) ADDRESSEE: Ratner & Prestia
     16
                  (B) STREET: P.O. Box 980
     17
                  (C) CITY: Valley Forge
     1.8
                  (D) STATE: PA
     19
                  (E) COUNTRY: USA
                                                             ENTED
     20
                  (F) ZIP: 19482
     21
             (V) COMPUTER READABLE FORM:
     23
                  (A) MEDIUM TYPE: Diskette
     24
                  (B) COMPUTER: IBM Compatible
     25
                  (C) OPERATING SYSTEM: DOS
     26
                  (D) SOFTWARE: FastSEQ for Windows Version 2.0
     27
            (vi) CURRENT APPLICATION DATA:
     29
                  (A) APPLICATION NUMBER: US/09/961,201
C-->30
                  (B) FILING DATE: 24-Sep-2001
C--> 31
                  (C) CLASSIFICATION:
     32
           (vii) PRIOR APPLICATION DATA:
     34
                  (A) APPLICATION NUMBER: 09/300,328
     36
                  (B) FILING DATE:
     37
                  (A) APPLICATION NUMBER: US/08/852,936
     39
                  (B) FILING DATE: 08-MAY-1997
     40
                  (A) APPLICATION NUMBER: 60/018,961
     42
                  (B) FILING DATE: 05-JUN-1996
     43
                  (A) APPLICATION NUMBER: 60/020,344
     45
                  (B) FILING DATE: 23-MAY-1996
     46
                  (A) APPLICATION NUMBER: 60/017,949
     48
                  (B) FILING DATE: 20-MAY-1996
     49
          (viii) ATTORNEY/AGENT INFORMATION:
     51
                  (A) NAME: Prestia, Paul F
     52
                  (B) REGISTRATION NUMBER: 23,031
     53
                   (C) REFERENCE/DOCKET NUMBER: p50483-2
     54
            (ix) TELECOMMUNICATION INFORMATION:
     56
                   (A) TELEPHONE: 610-407-0700
     57
                   (B) TELEFAX: 610-407-0700
     58
                   (C) TELEX: 846169
     59
     62 (2) INFORMATION FOR SEQ ID NO: 1:
             (i) SEQUENCE CHARACTERISTICS:
     64
                   (A) LENGTH: 416 amino acids
     65
```

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66 (B) TYPE: amino acid																
67	67 (C) STRANDEDNESS: single															
68																
70	GEO TO NO. 1.															
72	(	(xi)	SEQU	JENCE	DES	CRIF	OIT	I: SE	EQ II	O NO:	1:	_	_	<b>-</b>	3	T
74	Met	Asp	Glu	Ala	Asp	Arg	Arg	Leu	Leu		Arg	Cys	Arg	Leu	Arg	Leu
75	1				5					10	_	1	-	T	15	7
76	Val	Glu	Glu	Leu	Gln	Val	Asp	Gln		Trp	Asp	vaı	ьeu	Leu	ser	Arg
77				20					25				_	30	<b>a</b> 1	G =
78	Glu	Leu	Phe	Arg	рrо	His	Met		Glu	Asp	lle	GIn	Arg	Ата	GTÄ	ser
79			35				_	40		_	1	-1-	45	т	C1	mb ~
80	Gly	Ser	Arg	Arg	Asp	Gln		Arg	GIn	Leu	TTE	TTE	ASP	ьеи	GIU	1111
81		50			_		55	_	-1	<b>-</b> 1-	<b>a</b>	60	T 011	Clu	7 an	Thr
82	Arg	Gly	Ser	Gln	Ala		Pro	Leu	Pne	ше	ser	Cys	Leu	GIU	ASP	80
83	65					70	_	51.	<b>.</b>	3	75	7 an	7 mar	Cln	λla	
84	Gly	Gln	Asp	Met		Ala	Ser	Pne	ьeu	Arg	THE	ASII	Arg	GTII	95	GIY
85					85	_,	_	<b>01.</b>	3	90	mhw	Dwo	Val	37 <b>a</b> 1		Δνα
86	Lys	Leu	Ser	Lys	Pro	Thr	Leu	GIU	ASI	Leu	THE	PIO	Val	110	пец	ALG
87		_		100	_	_	<b>a</b> 1	77 7	105		Dro	Clu	Thr		Δτα	Pro
88	Pro	Glu		Arg	Lys	Pro	GIU		ьeu	Arg	PIO	GIU	125	FIU	пту	110
89	_		115		_	<b>~1</b>	<b>a</b> 1	120	C1	7 an	Wa 1	C137		T.011	Glu	Ser
90	Val			Gly	ser	GLY		Pne	СТУ	ASP	Val	140	Ата	шеи	Giu	DCI
91		130	-1	Asn		3	135	717	Пттас	Tlo	Lon		Mot	Glu	Pro	Cvs
92			GIY	Asn	Ala		ьeu	Ата	1 1 1	TTE	155	DCI	1100	O.L.		160
93	145	77.2	<b>a</b>	Leu	т1 о	150	λan	λen	Val	Δsn		Cvs	Arσ	Glu	Ser	
94	GLY	HIS	Cys	ьеи	165	116	ASII	ASII	Val	170	1 110	O <sub>I</sub> D	5		175	1
95	т	7 ~~	mh.~	Arg	TOS	Glv	Ser	Δgn	Tle		Cvs	Glu	Lvs	Leu	Arg	Arg
96	ьeu	ALY	1111	180	1111	GIY	DCI	11511	185		010		-1-	190	,	_
97 98	λνα	Dho	Cor	Ser	Ι.Δ11	His	Phe	Met			Val	Lvs	Gly	Asp	Leu	Thr
99	ALG	PHE	195		БСи	1115	1 110	200				-	205	-		
100	ז א	a T.v	e Lv	s Mei	t Va	l Lei	1 Al	a Le	u Le	u Gl	u Le	u Ala	a Ar	g Gl	n As	p His
101		a by 21		5 110			21					22	0			
102	G1	v Al	a Le	ıı Ası	o Cv	s Cv	s Va	l Va	l Va	1 11	e Le	u Se	r Hi	s Gl	у Су	s Gln
103	22	5				23	0				23	5				240
104	Αl	a Se	r Hi	s Lei	u Gl	n Ph	e Pr	o Gl	y Al	a Va	1 Ty	r Gl	y Th	r As	p Gl	y Cys
105					24	5				25	0				25	5
106	Pr	o Va	l Se	r Va	1 Gl	u Ly	s Il	e Va	l As	n Il	e Ph	e As	n Gl	y Th	r Se	r Cys
107				26	0				26	5				27	0	
108	Pr	o Se	r Le	u Gl	y Gl	y Ly	s Pr	о Гу	s Le	u Ph	e Ph	e Il	e Gl	n Al	а Су	s Gly
109			27	5				28	0				28	5		
110	Gl	v Gl	u Gl	n Ly	s As	p Hi	s Gl	y Ph	e Gl	u Va	1 Al	a Se	r Th	r Se	r Pr	o Glu
111		29	0				29	5				30	0			
112	As	p G]	u Se	r Pr	o Gl	y Se	r As	n Pr	o Gl	u Pr	o As	p Al	a Th	r Pr	o Ph	e Gln
113	30	5				31	0				31	5				320
114	Gl	u G]	y Le	u Ar	g Th	r Ph	e As	p Gl	n Le	eu As	p Al	a Il	e Se	r Se	r Le	u Pro
115					32	5				33	0				33	5
116	Th	r Pı	o Se	r As	p Il	e Ph	e Va	l Se	r Ty	r Se	r Th	r Ph	e Pr	o Gl	y Ph	e Val
117				34					34	5				35	U	

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201 TIME: 12:18:53

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118				_	_	_	_	<b>a</b> 1		<b></b>	m	17- 1	<b>a</b> 1	mh	т	3	
Asp   Ile Phe Glu Gln Trp Ala His Ser Glu Asp   Leu Gln Ser Leu Leu   370   375   375   380   380   380   395   400   400   415   385   390   395   400   415		Ser Trp		Asp	Pro	ьуs	ser		ser	тгр	TAL	Val		TIIL	теп	ASP	
121				<b>a</b> 1	<b>a</b> 1	т	31-		<b>a</b>	<b>61.</b>	N a m	T 011		C02	Lou	T 011	
Leu Arg Val Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met  123		=	Pne	GIU	Gin	ттр		HIS	ser	GIU	ASP		GIII	ser	Leu	ьец	
124			1	- 1 -		.1.		C = m	17.0.1	T	C1		Фит	Tvc	Cln	Mot	
405 400 415  27 (2) INFORMATION FOR SEQ ID NO: 2: 28 (i) SEQUENCE CHARACTERISTICS: 30 (A) LENGTH: 1578 base pairs 31 (B) TYPE: nucleic acid 32 (C) STRANDEDNESS: single 33 (D) TOPOLOGY: linear 35 (ii) MOLECULE TYPE: cDNA 36 (CCATGGGC ARGCGGATCCG GGGGTGCCGGCT GGTGGAAGAG GCCCATATG GCCCCATATG GCCCATATG GCCCATATG GCCCATATG GCCCCATATG GCCCA		_	vaı	Ата	Asn		vai	ser	Val	ьуѕ		116	1 7 1	цуз	GIII		
125			_	_,	_		<b>.</b>	3	T	T	-	nho	nho	T 170	Пhъ		
(2) INFORMATION FOR SEQ ID NO: 2:  129 (i) SEQUENCE CHARACTERISTICS: 130 (A) LENGTH: 1578 base pairs 131 (B) TYPE: nucleic acid 132 (C) STRANDEDNESS: single 133 (D) TOPOLOGY: linear 135 (ii) MOLECULE TYPE: CDNA 137 (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2: 138 GCCAGGAGGA GAGCGGATCG GCGGGTCCTG CGGGGGTGCC GGCTGCGGCT GGTGGAAGAG 140 CTGCAGGTGG ACCAGCTCTG GGACGTCCTG CTGAGCCGG AGCTGTTCAG GCCCCCATATC 141 ATCGAGGACA TCCAGCGGGC AGGCTCTGG TCTGAGCCGG AGCTGTCTAG GCACCTAGTC 142 ATAGATCTGG AGACTCAGGG GAGTCAGGT CTTCCTTTGT TCATCTCCTG CTTAGAGGAC 143 ACAGGCCAGG ACATCCTGGC TTGCTTTTCTG CGAACTAACA GCCAAGCAGG AAACTCTCTG 144 AAGCCAACC TAGAAAACCT TACCCCAGGT GTGCTCAGAC CAGAGATGG AAACTCAGAG 145 GTTCTCAGAC CGGAACACAC CAGACCAGG GAACTAGCTG 146 GGTGCTCTTC AGACTTTCAG GGGAAATGGA TTGCCCAGAGG 147 TGTGGCCACT GCCTCATATT CAACAATGTG ACATCTCTCG CGTGCTCCG CCCCATATC 148 CGCACTGGCT CCAACATCGA CTGTGAGAGA TCCTCGAGC 149 ATGGTGCAGA CACCACTCCA CTGTGAGAGA TTGCCCCAGTG 140 CGCACTGGCT CCAACATCGA CTGTGAGAGA TTGCCCCAGTG 141 TGTGCCCACT GCCAGAGTCC CAGACAAGAG 142 ATGGTGCAGA CACCACTCC CTTGGAGAGA TTGCCCCATGC 143 ATGGTGCAGA CCCCAATACC CAGACCAGTG CAACACAGAG 144 CCACCTCCC CCAACATCGA CTGTGAAGAG TTGCCCCATTC 146 CGCACTGCC CCAACATCCA CTGTGAAGAG TTGCCCCAGCC 147 TGTGCCCACT GCCAACATCCA CAGAAAATGG TCCTGCCTCC CCTCGCACC 148 CGCACTGCC CCAACATCCA CTGTGAAGAG TTGCCCCACCC 149 ATGGTGGAAG TTGTGAACAT CTTCAATGGA ACATCTCCC GCTCCTCCC CCCCCCCCC 140 ATGGTGGAAGA TTGTGAACAT CTTCAATGGA ACACACCAGTG TCCTGCCTCC CACCACTCCC 150 CAGGAAGAT TTGTGAACAT CTTCAATGGA ACACACCAGTG TCCTGCCC CACCACTCC 151 CAGGCCAGC ACCTCCACTTC CCCAGGGGG GAGAAAAAATTGA TCCTGTTCC TCACGCCC CAGCACACTCC CCCCCCTGC 152 CAGGAAGAT TTCATCCAGGC CTGTGGTGG GAGCAGAAA ACCATGGGTT TGAGGTGCC 153 AAGCCTCTTT TCATCCAGGC CTGTGGTGG GAGCAGAAA ACCATGGGTT TGAGGTGCC 154 CACCCCTTT TCATCCAGCC CAGACATAC CTAGTTTCC TCACCCCCAGC 1020 154 TCCACTTCC CTGAAGACA CTCCCAGCT GACCACATAC CTAGTTTCC TCACCCCCAGCT 1020 155 CAGGAAGGT TGAGGACCAT CTCCAACCACT TCCACCCCTGC TACACCAGAT CTAGACCACCCCT TCCACCCCCCCCCC		Pro Gly	Cys	Pne		Pne	ьeu	Arg	гаг		ьец	Pile	Phe	пуs		261	
(i) SEQUENCE CHARACTERISTICS:  (ii) MITYPE: nucleic acid  (ii) MOLECULE TYPE: cDNA  (iii) MOLECULE TYPE: cDNA  (ii) MOLECULE TYPE: cDNA  (iii) MOLECULE TYPE: cDNA  (iv) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  139 GCCATGGACG AAGCGGATCG GCGGCTCCTG CGGCGGTGCC GGCTGCGGCT GGTGGAAGAG (ACATGGAGACG ACAGCGCTG GCACCTCCTG CTGAGCCGCG AGCTGTTCAG GCCCCATATG (ACACGCTGG ACCAGCTCTG GACCAGCTCTG CTGAGCCGCG AGCTGTTCAG GCCCCATATG (ACACGCTGG ACACGCGGAGACACACC CAGACCAGGAGACACACC CAGACACACAC	125																
(A) LENGTH: 1578 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear  (X) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  (X) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  (X) SEQUENCE CHARACTERISTICS:  (X) SERVINDEDNESS: Single																	
(C) STRANDEDNESS: single  (A) EQUIPMENT STRANDEDNESS: single  (A) EQUIPMENT STRANDEDNESS: single  (A) EQUIPMENT STRANDEDNESS: single  (A) SCRACAGGGC CHARCACACH SINGLA CACACACH SINGLA CACACACH CACACACH SINGLA CACACACH CACACACH CACACACH CACACACH CACACACH CACACACH CACACH CA																	
(C) STRANDEDNESS: single  (3) (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  (xii) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  (xii) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  (xii) SEQUENCE CHARACTERISTICS:  (xii) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  (xii) SEQUENCE CHARACTERISTICS:  (xii) TOPOLOGY: TITCH Cold Calculum and cold cold cold cold cold cold cold col	· ·																
133	= = = · · · · · · · · · · · · · · · · ·																
(ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  139 GCCATGGACG AGAGGGATCG GCGGCTCCTG CGGCGGTGCC GGCTGCGGCT GGTGGAAGAG AGCGGATCG GGGCGTCCTG CTGAGCCGC AGCTGATCG GCCCCATATG 120  140 CTGCAGGTGG ACCAGCTCTG GGACGTCCTG CTGAGCCGC AGCTGATCG GCCCCATATG 120  141 ATCGAGGACA TCCAGCGGGC AGCTCTGGA TCTCGGCGG ATCAGGCCCAG GCACCTGATC 180  142 ATAGATCTGG AGACTCGAGG GAGTCAGGCT CTTCCTTTCTT TCATCTCCTG CTTAGAGGAC 240  143 ACAGGCCAAGC ACATGCTGGC TTCGTTTCTG CGAACTAACA GGCAAGCAGG AAAGTTGCC 300  144 AAGCCAACCC TAGAAAACCT TACCCCAGTG GTGCTCAGAC CAGAGATTCG CAAACCAGAG 360  145 GTTCTCAGAC CGGAAACACC CAGACCAGTG GACATTGGCT ACATCCAGGC CAGAGATTCG CAAACCAGAG 360  146 GGTGCTCTTG AGAGTTTGAG GGGAAATCAC GATTTGGCT ACATCCTGAG CATGGAGCCC 480  147 TGTGGCCACT GCCTCATTAT CAACAATGTG AACTTTGCCT GTTTCTCCTG GCTCTCTCTC GCTCGATCC AGACCAGG TGAGGGGCC CTGACACCAG TGGCTCCAACCAGG TGAGAGGCC AGAAACAAC GAACAACC AAAAAAATGT ACATCTGCC GCTCCTCTCTC GCTCATTTC 600  149 ATGGTGGAAGG TGAAGGGGGA CCTGACTGCC AAGAAAAATG TCCTGGAGAGCC AGACAACCAG ACCACGGCA CCTGCACCC AAGAAAAATG TCCTGCAGACC CAAGCCAGGC CCTCGCACC AGAAAAAATG TCCTGCAGACAC ACCAGGTGC TCCAAGCAGG TCCCAAGCCAGG CCTCTCTCCT CTCCTGCTTTC GCTGGAGTG CAACCACAGAC ACCTGCAGC ACCTGCAGC ACCTGCAGC ACCAGGTGC CCAAGCCAGG CCAAGCCCGGC CTGCAGCC AGAAAAAAATG TCCTTGAGAAAA ACCATGGG TCCAAGCAGG ACCACGGTGC CTGAGTGC CAAGCAGAAAAAATG TCCTGCAGAGACAC CAAGAACACC AAGAAAAATG TCCTGCAGGC ACCAGGTGC CAAGCCCAGG ACGAGAAAA AACCATGGGT TCCAGGCAC ACCTGCAGC CCAGGCCTTTCCC CAAGACACAC ACCCAGGT CCAAGCCCAGG ACGCAGAAAAAAAAAA																	
(Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  139 GCCATGGACG AAGCGGATCG GCGGCTCTCT GGGCGGTCC GGCTGGGCT GGTGGAAGAG GAGCTGTG GAGCGACCG GGCTGCTCT GTGAGCCGG GGCTTCAGG GCCCCATATG 120  140 CTGCAGGTGG ACCAGCTCTG GGAGCTCTG CTGAGCCGGG ACCTGTTCAG GCCCCATATG 120  141 ATCGAGGACA TCCAGCGGC AGCTCTGGA TCTCGGCGG ACCTGTTCAG GCCCCATATG 120  142 ATAGATCTGG AGACTCGAGG GAGTCAGGCT CTTCCTTTTT TCATCTCCTG CTTAGAGGAC 240  143 ACAGGCCAGG ACATGCTGGC TTCGTTTCTG CGAACTAACA GGCAAGCAGG AAAGTTGTCG 300  144 AAGCCAACCC TAGAAAAACCT TACCCCAGTG GTGCTCAGAC CAGAGCAGG AAAGTTGCC 420  145 GTTCTCAGAC CGGAAACACC CAGACCAGT GTGCTCAGAC CAGAGCAGG AAAGTTGCC 420  146 GGTGCTCTTG AGAGTTTGAG GGGAAATGCA GATTTGGCT ACATCCTGAG CATGGAGCCC 480  147 TGTGGCCACT GCCTCATTAT CAACAATGTG AACTTCTGC GTGAGTCCG GCTCCGCACC 540  148 CGCACTGGCT CCAACATCGA CTGTGAGAAG TTGCGGCCT GTGAGTCCG GCTCCGCACC 540  149 ATGGTGGAGG TGAAGGGGA CTCGACTGCC AGAAAATGG TCCTGGTTT GCTGGAGGTT 660  150 GCGCGCAGCA ACCACGGTG TCTGGACTAG TCCTGTGTTC TCACGGCTT 720  151 CAGGCCAGC ACCTGCAGTT CCTAGGAGGT TCCTCTCCT GCTGATTCT CTCAGGCTGT 720  152 GTCGACAGAA TTGTGAACAT CTTCAATGGG ACCACTGCC CAGACCAGG ACCACGGTT CCTGAGGCGC AGAACAGAG ACCACGGTT CCTGAGGCGC CAGACCAGT TCCTCT TCACGGCTT 720  151 CAGGCCAGC ACCTGCAGT CCCAGGGGCT GTCTACGGC CAGACTGGC CCTGTGTGT 780  152 GTCGACAAGA TTGTGAACAT CTTCAATGGG ACCACTGCC CAGACTGGC CAGACTGGC CACCCCGTTC 780  153 AAGCTCTTTT TCATCCAGGC CTGTGGTGGG GACCAGAAA ACCATGGGTT TGAGGTGGC  900  154 TCCACTTCC CTGAAGACGA GTCCCTTGG GAGCCAATT CTAGTTTGC CACCCCGTC 960  155 CAGGAAGGTT TGAGGACCT CACCTGACAC ATCTTTCAC AGCCCAGAGC CACACCAGT 1020  156 GCCCCTCGT ACCTTGAGAC CCTGGCAAT GCTCTTTTAGC CACCCCGTTC 760  157 GGCTCCTGGT ACCTTGAGAC CCTGGCCAAT GCTTTTTAGC ACCAGAGGAT TCATTTTAACCAG 120  158 CTCCCTGGT GCTTTAATTT CCTCCGGAAA AACTTTTCT TTAAAACAT ATAAGGCCA 1140  158 CTCCCTGGT GCTTTAATTT CCTCCGGAAA AACTTTTCT TTAAAACAT ATAAGGCCA 1140  157 GCCCCCAGC TGCTCTTATCTG CACCTAAT TCTCTTCT TTAAAACAT ATAAGGCCA 1140  160 GGCCCCCCAC CCTGCCTTAT CTTGACCACC AAGCTTTCCT TCAGAGCT TCATTTCTT TTAAACAG 1200  161 CTGAGGCTG GACTTCCTG CAACTCAGAT TCCTCTCTGAGAT TCCTC								ar									
139 GCCATGGACG AAGCGGATCG GCGGCTCCTG CGGCGGTCC GGCGGCGCG GGTGGAAGAG 6 140 CTGCAGGTGG ACCACTCTG GGACGTCTG ACCACGCGG ACCACTATG 120 141 ATCGAGGACA TCCAGCGGGC AGCCTCTGAA TCCAGCGGG ATCAGGCCAG GCCCATATG 180 142 ATAGATCTGG AGACTCTGAG CAGCCCTTGAA TCTCCGCGGG ATCAGGCCAG GCCCATATG 180 144 AAGCCAACC TAGAAAACCT TACCCCAGTG GGACATACA GGCAAGCAGG AAAGTTCTCG 144 AAGCCAACC TAGAAAACCT TACCCCAGTG GTGCTCAGAC CAGAGCAGG AAAGTTCTCG CAAACCAGAG 360 145 GTTCTCAGAC CGGAAAACCC CAGACCAGTG GACATTGGTT CTGAGAGATT CGGTGATTCT CAGACCACTG GACATTGGCT CAAACCAGAG 360 147 GTTCTCAGAC CGGAAAACCC CAGACCAGTG GACATTGGCTT CTGAGAGATT CGGTGATTCT CAACACTGCT CCACACTATA CAACATGTG ACATCTCTCC GTGAGTCC CAACACCACG GGGAAATGC CAAACCACGAC CTGAGAAACCC CAGACATGG GACATTGGCT ACATCCTCAG CATGGAGACT CAACACTCTGC CAAACATCCA CTGTGAGAAG TTGCGCGCTC GCTCCTCCT CAACACTGCC CAAACACTCCA CTGTGACAAG TTGCGCGCTC GCTCCTCCT CAACACTGCC CAAACACTCCA CTGTGACAAG TTGCGCGCTC GCTCCTCCTC GCTGCACC CAACACTGCC CCACACTGC TCTGGACTGC TCGCTGCTCC GCTGCACC CAACACGGAG ACCACGGTC TCTGGACTGC TGCGTGGTG TCATTCTCT TCACGGCTGT TCAGGCAAG ACCACGGTC TCTGGACTGC TGCGTGGTG TCATTCTCT TCACGGCTGT TCAGGCCA CAGAGAGAAG ACCACGGTC TCTGAATGG ACCACGTGC CAGAGAGAAG ACCACGGTG TCTCAAAGAG ACCACGGTG TCTCAAAGACA ACCACGGTG TCACACCCAGTG AGGAAAAAC ACCATGGGT TTGAGGAAAAC ACCACGGTG TTGAGAAAA ACCATGGGT TTGAGGAAAACCCC AGACGAAGAAAAAAAAAA								M. O		NO.							
140 CTGCAGGTGG ACCAGCTCTG GGACGTCTG CTGAGCCGC AGCTGTTCAG GCCCCATTATG 141 ATCGAGGACA TCCAGCGGGC AGGCTCTGGA TCTCCGCGGG ATCAGGCCAG GCAGCTGATC 142 ATAGATCTGG AGACTCGAGG GAGCTCAGGCT CTTCCTTTGT TCATCCTCG CTTAGAGGAC 143 ACAGGCCAGG ACATCCTGCC TTCGTTTCTG CGAACTACA GGCAAGCAGG AAAGTTGTCG 144 AAGCCAACCC TAGAAAACCT TACCCCAGTG GTGCTCTAGAC CAGAGATTCG CAAACCAGAG 145 GTTCTCAGAC CGGAACACC CAGACCAGTG GTGCTCAGAC CAGAGATTCG CAAACCAGAG 146 GGTGCTCTTG AGAGTTTGAG GGGAATGCA GATTTGGTT CTGGAGGAT CGGTGATGTC 147 TGTGGCCACT GCCTCATTAT CAACAATGTG AACTTCTGCC GTGATGCC CAGGCCACC 148 CGCACTGGCT CCACACATCCA CTGTGACGAAG TTGCTGCCCACC GCTCCCACC 149 ATGGTGGAGG TGAAGGCCG CTGACTGCC CAGACAATGC CATGGAGGCC GCTCCCCACC 149 ATGGTGGAGG TGAAGGCCGA CTGGACTGCC CAGACATCCA CATGGAGCCC GCTCCCCCC 150 CGCGGCAGG ACCACGGTGC CTGGACACTCC CAGACAATGC TGCTGAGGATG TCCTCCTC GCTGCATTTC 151 CAGGCCACG ACCACGTGC CTGGACACTCC TGCGTGGGTG TCATTCCTC TCACGGCTGT 152 GTCGAGAAGA TTGTGAACAT CTCCAAGGG ACCACGGTGC CACACCTCG AGCAAGAGA ACCACGGTGC TCTCAATGGG ACCACGTGC CAGCCACC CAGCCCACC AGCCCACCC AGCCCACCC AGCCACACCC AGCCACACCC CTGTGCGG AGCACAAGAA ACCATGGGTT TCACTCGCACC AGCCACACCC AGCCACCCC CTGAAGACA TCCACCCAGT TCACTTCCC CTGAAGACA GTCCCCTGGC AGCAAAAAAAAAA		(X1)	SEQU	DENC	E DES	CRI	TOUR	N: 51	EO TI			CCCTT(	cccc	יחי כי	משכני	1 1 C 1 C	60
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147 TGTGGCCACT GCCTCATTAT CAACAATGTG AACTTCTGCC GTGAGTCCGG GCTCCGCACC 148 CGCACTGGCT CCAACATCGA CTGTGAGAAG TTGCGGCGTC GCTTCTCCTC GCTGCATTTC 600 149 ATGGTGGAGG TGAAGGCGA CCTGACTGCC AAGAAAATGG TGCTGGGTTT GCTGGACTGC 720 151 CAGGCCAGC ACCACCGATGC TCTGGACTGC TGCGTGGTG TCATTCTCTC TCACGGCTTG 720 151 CAGGCCAGCC ACCTGCAGTT CCCAGGGGCT GTCTACGGCA CAGATGGATG CCCTGTGTCG 780 152 GTCGAGAGA TTGTGGACAC CTTCAATGGG ACCAGCTGC CCAGGCTGC CCAGCCTGG AGGAAACCC ACCTCCAGC CTGTGTGG GAGCAGAAAG ACCACTGCAGA TCATCACGC CTGAAGACGA CTGCAGACC CTGAGAGAAAA ACCATGGGTT TGAGGTGGCC 900 154 TCCACTTCC CTGAAGACGA GTCCCCTGGC AGTAACCCCG AGCCAGATG CCCCCAGT 960 155 CAGGAAGGTT TGAGGACCT CGACCAGCTG GACCACATAT CTAGTTTGCC CACACCCAGT 1020 156 GACATCTTTG TGTCCTACTC TACTTTCCCA GGTTTTGTTT CCTGGAGGAC CCCCAAGAGT 1020 157 GGCTCCTGGT ACGTTGAGAC CCTGGACGAC ATCTTTGAGAC AGTGGGCTC CCCCAAGAGT 1080 158 CTGCAGTCCC TCCTGTAGAGAC CCCCGAAAAA AAACTTTTCT TTAAAACAAC 1200 159 ATGCCTGGT GCTTTAATTT CCTCCGGAAA AAACTTTTCT TTAAAACATC ATAAGGCCAG 1260 160 GGCCCCTCAC CCTGCCTTAT CTTGCACCC AAAGCTTTCC TGCCCAAGAGT TTATAAACAG 1200 161 CTGAGGCCT GACTTCTCT CAACCACC AAGCTTTCC TGCCCAAGAGT TTAAAACATC ATAAGGCCAG 1260 162 CTCTGCAGT GACAGACAGG CTCTTAGCAG CTCTTGAGAC CTCCAAAAGAG TCTGCTCTTTT 1380 162 CTCTGCCAGT GACAGACAGG CTCTTAGCAG CTCTCAGATT GACGACAAGT CTCTGCTCTTT 1380 163 GGAGGAAGAG GGACAGATGA ATGCCGTGGA TTGCACCTA ACTGCACT TCCAGATT GACGACAAGT GCTGAACAGT 1500 164 CCAGGGCTAG TGACTTGGTG TCCCATGATC CTCTCAGATT GACGACAAGT GCTGAACAGT 1500 164 CCAGGGCTAG TGACTTGGTG TCCCATGATC CTCTCAGATT GACGACAAGT GACGACAAGT ATGCCGTGGA TTGCACCTA ACTGCACT TCCAGATT GACGACAAGT GACGACAAGT ATGCCGTGGA TTGCACCTA ACTGCACT TCCAGATT GACGACAAGT GACTTCTTT 1380 165 CCTCTGCACT ACTGCACT TCCCATGATC CTCTGTTTGACA CTTCCAGATT GACGACAAGT GACGACAAGT ATGCCGTGGA TTGCACTTTGACA CTTCCAGATT GACGACAAGT GACGACAAGT ATGCCGTGAACAGT TCTCCAGATT TCCCAGATT TCCT	145	GTTCTCAG	AC CO	jGAA/	ACACC	CAC	JACCA	AGIG	CARC	DDCC(	יייייי זוז י	CIGGI	100A. 10TC	AG C	ATCC:	ACCCC	
148 CGCACTGGCT CCAACATCGA CTGTGAGAAG TTGCGGCGTC GCTTCTCCTC GCTGCATTC 149 ATGGTGGAGG TGAAGGGCGA CCTGACTGCC AAGAAAATGG TGCTGGCTTT GCTGGAGCTG 150 GCGCGGCAGG ACCACGGTGC TCTGGACTGC TGCGTGGTG TCATTCTCTC TCACGGCTGT 720 151 CAGGCCAGCC ACCTGCAGTT CCCAGGGGCT GTCTACGGCA CAGATGGATG CCCTGTGTCG 780 152 GTCGAGAAGA TTGTGAACAT CTTCAATGGG ACCAGCTGCC CCAGCCTGGG AGGGAAGCCC 840 153 AAGCTCTTTT TCATCCAGGC CTGTGGTGG GAGCAGAAAG ACCATGGGTT TGAGGTGGCC 900 154 TCCACTTCC CTGAAGACGA GTCCCCTGGC AGTAACCCCG AGCCAGTGC CACCCCGTTC 960 155 CAGGAAGGTT TGAGGACCTT CGACCAGCTG GACGCATAT CTAGTTTGCC CACACCCAGT 1020 156 GACATCTTG TGTCCTACTC TACTTTCCCA GGTTTTGTT CCTGGAGGGA CCCCAAGAGT 1080 157 GGCTCCTGGT ACGTTGAGAC ATCTTTGAGC AGTGGGCTCA CTCTGAAGAC 1140 158 CTCCAGTCC TCCTGCTTAG GGTCGCTAAT GCTGTTTCG TAAAAAGAGA CCCTGAAGAC 11200 159 ATGCCTGGT GCTTTAATTT CCTCCGGAAA AAACTTTCT TTAAAACATC ATAAGCCAG 1260 160 GGCCCCTCAC CCTGCCTTAT CTTGCACCC AAAGCTTTCC TGCCCCAGGC CTGAAAGAGG 1260 161 CTGAGGCCTG GACAGACAG CTCTTAGCAC ATTTTCAGC CGGCACAGG CTCAAAAGAGG 1260 162 CTCTGCCAGT GACAGACAG CTCTTAGCAC ACTTCAGAT GACGACAAGT GACTGACTTT CTGCACCCC AAACCTTTCC TGCCCCAGGC CTGAAAAGAGG 1260 163 GGAGGAAGAG GACAGACAG CTCTTAGCAC CTTCCAGATT GACGACAAGT GACTGCTTTT 1380 164 CCAGGGCTAG TGACTTGGTG TCCCATGAT CCTCCAGATT GACGACAAGT GACGACAAGT 1440 165 CCTCTGCCAGT TACTTGGTG TCCCATGATC CCTGTGTTGG TCTCTTTAGACAC ACGGACAAGT GACTGACAT 1500 164 CCAGGGCTAG TGACTTGGTG TCCCATGATC CCTGTGTTGG TCTCTTAGACA ACGTTTGTAGC AGGGACAAGT GACTGACAT 1500 165 CCTCTGCACT ACTGACAT 1500 166 CCCTCTGCACT ACTGACAT 1500 167 (2) INFORMATION FOR SEQ ID NO: 3: 169 (i) SEQUENCE CHARACTERISTICS: 170 (A) LENGTH: 639 base pairs 171 (B) TYPE: nucleic acid 172 (C) STRANDEDNESS: single	146	GGTGCTCT	TG AC	JAGT.	TTGAC	יטט נ	JAAA:	TGCA	GAT	TTGG(		CTCA	201GE	ic c	CTCC(	CACC	
149 ATGGTGGAGG TGAAGGGCGA CCTGACTGCC AAGAAAATGG TGCTGGCTTT GCTGGAGCTG 150 GCGCGCAGG ACCACGGTGC TCTGGACTGC TGCGTGGTG TCATTCTCTC TCACGGCTGT 720 151 CAGGCCAGCC ACCTGCAGTT CCCAGGGGCT GTCTACGGCA CAGATGGAATG CCCTGTGTCG 780 152 GTCGAGAGAA TTGTGAACAT CTTCAATGGG ACCAGCTGCC CCAGCCTGGG AGGAAGCCC 840 153 AAGCTCTTT TCATCCAGGC CTGTGGTGG GAGCAGAAAG ACCATGGGTT TGAGGTGGCC 900 154 TCCACTTCCC CTGAAGACGA GTCCCCTGGC AGTAACCCCG AGCCAGATGC CACCCCGTTC 960 155 CAGGAAGGTT TGAGGACCTT CGACCAGCTG GACGCCATAT CTAGTTTGCC CACACCCAGT 1020 156 GACATCTTTG TGTCCTACTC TACTTTCCCA GGTTTTGTTT CCTGGAGGGA CCCCAAGAGT 1080 157 GGCTCCTGGT ACGTTGAGAC CCTGGACGAC ATCTTTGAGC AGTGGGTCA CTCTGAAGAC 1140 158 CTGCACTCC TCCTGCTTAG GGTCGCTAAT GCTGTTTCG TGAAAGAGCA 1200 159 ATGCCTGGT GCTTTAATTT CCTCCGGAAA AAACTTTCT TTAAAACATC ATAAGACCAG 1200 160 GGCCCCTCAC CCTGCCTTAT CTTGCACCCC AAAGCTTTCC TGCCCAGGC CTGAAAGAGG 1320 161 CTGAGGCCTG GACTTTCCT CACACCAAGA ATCTTTGAAC CGGCACAGG TCTGCTCTTT 1380 162 CTCTGCCAGT GACAGACAGG CTCTTAGCAG ACTTTGAAC CGGCACAAGT GCTGAAAGAGG 1320 163 GGAGGAAGAG GGACAGATGA ATGCCGTGGA TTGCACGCG CTGAAAGAGG 1320 164 CCAGGGCTAG TGACTTGCTG CACACCAGATC CCTGCAGAC ACTCTCTTT 1380 165 CCTCTGCAGT ACTGACAT CCCATGATC CCTGTGTTGG TCCCATGAG ACTGCTCTTT 1380 166 CCCCTGCACT ACTGACAT CCCCATGATC CCTGTGTTGG TCCCATGAG ACTGCTGTT 1500 167 (2) INFORMATION FOR SEQ ID NO: 3: 169 (i) SEQUENCE CHARACTERISTICS: 170 (A) LENGTH: 639 base pairs 171 (B) TYPE: nucleic acid 172 (C) STRANDEDNESS: single	147	TGTGGCCA	CT GO	CCTC	ATTAT	CAR	ACAA:	TGTG	MMC/	7000		CCTT	31 CCC	יט טי	CTCC	A THE THE	
150 GCGCGCAGG ACCACGGTGC TCTGGACTGC TGCGTGGTGG TCATTCTCTC TCACGGCTGT 720 151 CAGGCCAGCC ACCTGCAGTT CCCAGGGGCT GTCTACGGCA CAGATGGATG CCCTGTGTCG 780 152 GTCGAGAAGA TTGTGAACAT CTTCAATGGG ACCAGCTGCC CCAGCCTGGG AGGGAAGCCC 840 153 AAGCTCTTTT TCATCCAGGC CTGTGGTGGG GAGCAGAAAG ACCATGGGTT TGAGGTGGCC 900 154 TCCACTTCCC CTGAAGACGA GTCCCCTGGC AGTAACCCCG AGCCAGATGC CACCCCGTTC 960 155 CAGGAAGGTT TGAGGACCAT CGACCAGCTG GACGCCATAT CTAGTTTGCC CACCCCGGTC 960 156 GACATCTTTG TGTCCTACTC TACTTTCCCA GGTTTTGTTT CCTGGAGGAG CCCCAAGAGT 1020 157 GGCTCCTGGT ACGTTGAGAC CCTGGACGAC ATCTTTGAGC AGTGGGCTCA CTCTGAAGAC 1140 158 CTGCAGTCCC TCCTGCTTAG GGTCGCTAAT GCTGTTTCG TGAAAGGGAT TTATAAACAG 1200 159 ATGCCTGGT GCTTTAATTT CCTCCGGAAA AAACTTTTCT TTAAAACATC ATAAGGCCAG 1260 160 GGCCCCTCAC CCTGCCTTAT CTTGCACCCC AAAGCTTTCC TGCCCCAGGC CTGAAAGAGG 1320 161 CTGAGGCCTG GACTTTCCTG CAACTCAAGG ACTTTGAAGC CGGCACAAGT GCTGAACAGT 1440 162 CTCTGCCAGT GACAGACAGG CTCTTAGCAG CTTCCAGATT GACGACAAGT GCTGAACAGT 1440 163 GGAGGAAGAG GGACAGATGA ATGCCGTGGA TTGCACGTG ACTGCACAGG TCTGCTCTTT 1380 164 CCAGGGCTAG TGACTTGGTG TCCCATGATC CCTGTGTTG TCCCATGAGC AGTGGCTGGT 1500 165 CCTCTGCACT ACTGACAT TCCCATGATC CCTGTTTTG TCCCATGAGC AGTGGCTGGT TCCCATGATC 1500 166 CCTCTGCACT ACTGACAT TCCCATGATC CCTGTTTTG TCCCATGAGC AGTGGCTGGT TCCCATGACAT 1500 167 (2) INFORMATION FOR SEQ ID NO: 3: 169 (i) SEQUENCE CHARACTERISTICS: 170 (A) LENGTH: 639 base pairs 171 (B) TYPE: nucleic acid 172 (C) STRANDEDNESS: single	148	CGCACTGG	CT C	CAAC	ATCG	CTC	JUAN	TICCC	1100	א א א א ה א א א א ה	מוכ	TCCT/		יתי כי	CTGG	ACCTC	
151 CAGGCCAGCC ACCTGCAGTT CCCAGGGGCT GTCTACGGCA CAGATGGATG CCCTGTGTCG 152 GTCGAGAAGA TTGTGAACAT CTTCAATGGG ACCAGCTGCC CCAGCCTGGG AGGGAAGCCC 153 AAGCTCTTTT TCATCCAGGC CTGTGGTGGG GAGCAGAAAG ACCATGGGTT TGAGGTGGCC 154 TCCACTTCCC CTGAAGACGA GTCCCCTGGC AGTAACCCCG AGCCAGATG CACCCCGTTC 155 CAGGAAGGTT TGAGGACCTT CGACCAGCTG GACGCATAT CTAGTTTGCC CACACCCAGT 156 GACATCTTTG TGTCCTACTC TACTTTCCCA GGTTTTGTTT CCTGGAGGGA CCCCAAGAGT 157 GGCTCCTGGT ACGTTGAGAC CCTGGACGAC ATCTTTGAGC AGTGGGCTCA CTCTGAAGAC 1140 158 CTGCAGTCCC TCCTGCTTAG GGTCGCTAAT GCTGTTTCGG TGAAAGAGGAT TTATAAAACAG 1200 159 ATGCCTGGTT GCTTTAATTT CCTCCGGAAA AAACTTTTCT TTAAAAACATC ATAAGGCCAG 1320 160 GGCCCCTCAC CCTGCCTTAT CTTGCACCCC AAAGCTTTCC TGCCCCAGGG TCTGAAAGAGG 1320 161 CTGAGGCCTG GACATTCCTG CAACTCAAGG ACTTTGAAGC CGGCACAGGG TCTGCTCTTT 1380 162 CTCTGCCAGT GACAGACAGG CTCTTAGCAG CTTCCAGATT GACGACAGAG GCTGAACAGT 1440 163 GGAGGAAGAG GGACAGATGA ATGCCGTGGA TTGCACGTGG NCTCTTGAGC AGTGGCTGGT 1500 164 CCAGGGCTAG TGACTTGGTG TCCCATGATC CCTGTGTTGG TCTCTTAGCAG CAGGGATTAA 1560 165 CCTCTGCACT ACTGACAT CCCATGATC CCTGTGTTGG TCCCATGAT 1500 164 CCAGGGCTAG TGACTTGGTG TCCCATGATC CCTGTGTTGG TCTCTTAGCAG CAGGGATTAA 1560 165 CCTCTGCACT ACTGACAT 1570  (A) LENGTH: 639 base pairs 171 (B) TYPE: nucleic acid 172 (C) STRANDEDNESS: single	149	ATGGTGGA	GG TO	JAAG	36CG <i>E</i>	i mar	TGAC	CINCC	mcco	3888. 3866	rcc i	יים איטיני יים איטיני	TOTO	ייר ידי	CIGG	CCTCT	
152 GTCGAGAAGA TTGTGAACAT CTTCAATGGG ACCAGCTGCC CCAGCCTGGG AGGGAAGCCC 153 AAGCTCTTTT TCATCCAGGC CTGTGGTGGG GAGCAGAAAG ACCATGGGTT TGAGGTGGCC 900 154 TCCACTCCC CTGAAGACGA GTCCCCTGGC AGTAACCCCG AGCCAGATGC CACCCCGTTC 960 155 CAGGAAGGTT TGAGGACCTT CGACCAGCTG GACGCCATAT CTAGTTTGCC CACACCCAGT 1020 156 GACATCTTTG TGTCCTACTC TACTTTCCCA GGTTTTGTTT CCTGGAGGGA CCCCAAGAGT 1080 157 GGCTCCTGGT ACGTTGAGAC CCTGGACGAC ATCTTTGAGC AGTGGGCTCA CTCTGAAGAC 1140 158 CTGCAGTCC TCCTGCTTAG GGTCGCTAAT GCTGTTTCGG TGAAAGGGAT TTATAAACAG 1200 159 ATGCCTGGT GCTTTAATTT CCTCCGGAAA AAACTTTTCT TTAAAACAGT ATAAGCCAG 1260 161 CTGAGGCCTG GACTTTCCTG CAACTCAAGG ACTTTGAGC CGGCACAGG TCTGCTTTT 1380 162 CTCTGCCAGT GACAGACAG CTCTTAGAGA CTTCCAGATT GACGACAGG TCTGCTTTT 1380 163 GGAGGAAGAG GGACAGATGA ATGCCGTGGA TTGCACCG CGGCACAGG TCTGCTCTTT 1380 164 CCAGGGCTAG TGACTTGGT TCCCATGAT CTCCATGAT GACGACAAGT GCTGAACAGT 1440 163 GGAGGAAGAG GGACAGATGA ATGCCGTGGA TTGCACGTG NCTCTTGAGC AGTGGCTGGT 1500 164 CCAGGGCTAG TGACTTGGTG TCCCATGATC CCTGTTTGG TCTCTTGAGC AGTGGCTGGT 1500 165 CCTCTGCACT ACTGACAT CCCATGATC CCTGTTTGG TCCCATGATC ACTGACAGT 1500 165 CCTCTGCACT ACTGACAT 100:3:  169 (i) SEQUENCE CHARACTERISTICS:  170 (A) LENGTH: 639 base pairs  171 (B) TYPE: nucleic acid  172 (C) STRANDEDNESS: single	150	GCGCGGCA	GG A	CCAC	JOTU(		TOGA	CCCT	CTC	71GG.	ימט	בכתו. מאמאי	rcca.	ים מ	ייייייייייייייייייייייייייייייייייייי	TGTCG	
153 AAGCTCTTTT TCATCCAGGC CTGTGGTGGG GAGCAGAAAG ACCATGGGTT TGAGGTGGCC 154 TCCACTTCCC CTGAAGACGA GTCCCCTGGC AGTAACCCCG AGCCAGATGC CACCCCGTTC 960 155 CAGGAAGGTT TGAGGACCTT CGACCAGCTG GACGCCATAT CTAGTTTGCC CACACCCAGT 1020 156 GACATCTTTG TGTCCTACTC TACTTTCCCA GGTTTTGTTT CCTGGAGGGA CCCCAAGAGT 1080 157 GGCTCCTGGT ACGTTGAGAC CCTGGACGAC ATCTTTGAGC AGTGGGCTCA CTCTGAAGAC 1140 158 CTGCAGTCC TCCTGCTTAG GGTCGCTAAT GCTGTTTCGG TGAAAGGGAT TTATAAACAG 1200 159 ATGCCTGGT GCTTTAATTT CCTCCGGAAA AAACTTTTCT TTAAAACATC ATAAGGCCAG 1260 160 GGCCCCTCAC CCTGCCTTAT CTTGCACCCC AAAGCTTTCC TGCCCCAGGC CTGAAAGAGG 1320 161 CTGAGGCCTG GACTTCCTG CAACTCAAGG ACTTTGNAGC CGGCACAGGG TCTGCTCTTT 1380 162 CTCTGCCAGT GACAGACAGG CTCTTAGCAG CTTCCAGATT GACGACAAGT GCTGAACAGT 1440 163 GGAGGAAGAG GGACAGATGA ATGCCGTGGA TTGCACGTG NCTCTTGAGC AGTGGCTGGT 1500 164 CCAGGGCTAG TGACTTGGTG TCCCATGATC CCTGTGTTG TCTCTTGAGC AGTGGCTGGT 1500 165 CCTCTGCACT ACTGACAT 1660 (1) SEQUENCE CHARACTERISTICS:  167 (2) INFORMATION FOR SEQ ID NO: 3:  168 (i) SEQUENCE CHARACTERISTICS:  170 (A) LENGTH: 639 base pairs  171 (B) TYPE: nucleic acid (C) STRANDEDNESS: single	T2T	CAGGCCAG	CC A	CCTG	AGII	r ccc	UDDA.	BCCC	ACC:	A C C T C	CC	CAGA. CCAG	ገር መፈረ ግር ሞር (	IG A	CCTO.	AGCCC	
154 TCCACTTCCC CTGAAGACGA GTCCCCTGC AGTAACCCCG AGCCAGATGC CACCCCGTTC 155 CAGGAAGGTT TGAGGACCTT CGACCAGCTG GACGCCATAT CTAGTTTGCC CACACCCAGT 1020 156 GACATCTTTG TGTCCTACTC TACTTTCCCA GGTTTTGTTT CCTGGAGGGA CCCCAAGAGT 1080 157 GGCTCCTGGT ACGTTGAGAC CCTGGACGAC ATCTTTGAGC AGTGGGCTCA CTCTGAAGAC 158 CTGCAGTCCC TCCTGCTTAG GGTCGCTAAT GCTGTTTCGG TGAAAGGGAT TTATAAACAG 159 ATGCCTGGTT GCTTTAATTT CCTCCGGAAA AAACTTTTCT TTAAAACATC ATAAGGCCAG 160 GGCCCCTCAC CCTGCCTTAT CTTGCACCCC AAAGCTTTCC TGCCCCAGGC CTGAAAGAGG 161 CTGAGGGCCTG GACTTTCCTG CAACTCAAGG ACTTTGNAGC CGGCACAGGG TCTGCTCTTT 162 CTCTGCCAGT GACAGACAGG CTCTTAGCAG CTTCCAGATT GACGACAAGT GCTGAACAGT 163 GGAGGAAGAG GGACAGATGA ATGCCGTGGA TTGCACGTGG NCTCTTGAGC AGTGGCTGGT 164 CCAGGGCTAG TGACTTGGTG TCCCATGATC CCTGTGTTGG TCTCTTAGCAG CAGGGATTAA 165 CCTCTGCACT ACTGACAT 167 (2) INFORMATION FOR SEQ ID NO: 3: 168 (i) SEQUENCE CHARACTERISTICS: 170 (A) LENGTH: 639 base pairs 171 (B) TYPE: nucleic acid 172 (C) STRANDEDNESS: single	152	GTCGAGAA	GA II	TGTG	CACCO	CI.	TORR	TCCC	CACC	מטכוני מממגי	AAC	ACCA!	racar	יידי יידין	GDG/11	TGGCC	
155 CAGGAAGGTT TGAGGACCTT CGACCAGCTG GACGCCATAT CTAGTTTGCC CACACCCAGT 156 GACATCTTTG TGTCCTACTC TACTTTCCCA GGTTTTGTTT CCTGGAGGGA CCCCAAGAGT 157 GGCTCCTGGT ACGTTGAGAC CCTGGACGAC ATCTTTGAGC AGTGGGCTCA CTCTGAAGAC 158 CTGCAGTCCC TCCTGCTTAG GGTCGCTAAT GCTGTTTCGG TGAAAGGGAT TTATAAACAG 159 ATGCCTGGTT GCTTTAATTT CCTCCGGAAA AAACTTTTCT TTAAAACATC ATAAGGCCAG 160 GGCCCCTCAC CCTGCCTTAT CTTGCACCCC AAAGCTTTCC TGCCCCAGGC CTGAAAGAGG 161 CTGAGGCCTG GACTTTCCTG CAACTCAAGG ACTTTGNAGC CGGCACAGGG TCTGCTCTTT 162 CTCTGCCAGT GACAGACAGG CTCTTAGCAG CTTCCAGATT GACGACAAGT GCTGAACAGT 163 GGAGGAAGAG GGACAGATGA ATGCCGTGGA TTGCACCGTGG NCTCTTGAGC AGTGGCTGGT 164 CCAGGGCTAG TGACTTGGTG TCCCATGATC CCTGTGTTGG TCTCTAGGAG CAGGGATTAA 165 CCTCTGCACT ACTGACAT 167 (2) INFORMATION FOR SEQ ID NO: 3: 169 (i) SEQUENCE CHARACTERISTICS: 170 (A) LENGTH: 639 base pairs 171 (B) TYPE: nucleic acid 172 (C) STRANDEDNESS: single	T23	MAGCTCTT	77 T	CAIC	CAGGC	, CI(	יים מינים. מבים מינים	TCCC	A CT	A A C C (	התם . זרב	ACCC:	ነርዕር:	בר כ	3/100	CGTTC	
156 GACATCTTTG TGTCCTACTC TACTTTCCCA GGTTTTGTTT CCTGGAGGGA CCCCAAGAGT 157 GGCTCCTGGT ACGTTGAGAC CCTGGACGAC ATCTTTGAGC AGTGGGCTCA CTCTGAAGAC 158 CTGCAGTCCC TCCTGCTTAG GGTCGCTAAT GCTGTTTCGG TGAAAGGGAT TTATAAACAG 159 ATGCCTGGTT GCTTTAATTT CCTCCGGAAA AAACTTTTCT TTAAAACATC ATAAGGCCAG 160 GGCCCCTCAC CCTGCCTTAT CTTGCACCCC AAAGCTTTCC TGCCCCAGGC CTGAAAGAGG 161 CTGAGGCCTG GACTTTCCTG CAACTCAAGG ACTTTGNAGC CGGCACAGGG TCTGCTCTTT 1380 162 CTCTGCCAGT GACAGACAGG CTCTTAGCAG CTTCCAGATT GACGACAAGT GCTGAACAGT 1440 163 GGAGGAAGAG GGACAGATGA ATGCCGTGGA TTGCACGTGG NCTCTTGAGC AGTGGCTGGT 1500 164 CCAGGGCTAG TGACTTGGTG TCCCATGATC CCTGTGTTGG TCTCTAGGAG CAGGGATTAA 1560 165 CCTCTGCACT ACTGACAT 1578 167 (2) INFORMATION FOR SEQ ID NO: 3: 169 (i) SEQUENCE CHARACTERISTICS: 170 (A) LENGTH: 639 base pairs 171 (B) TYPE: nucleic acid 172 (C) STRANDEDNESS: single	154	CACCACTTC	MOTION TO	CACC	₃₩ĊĠ₽ ₩ĊĊͲŪ	י ככי	ACCA!	CCTG	GAC	מתכטי מררמי	יים מיז יים מיז	лоссі Стасі	TTTG(	7C C	ACAC	CCAGT	
157 GGCTCCTGGT ACGTTGAGAC CCTGGACGAC ATCTTTGAGC AGTGGGCTCA CTCTGAAGAC 1140 158 CTGCAGTCCC TCCTGCTTAG GGTCGCTAAT GCTGTTTCGG TGAAAAGGGAT TTATAAACAG 1200 159 ATGCCTGGTT GCTTTAATTT CCTCCGGAAA AAACTTTTCT TTAAAACATC ATAAGGCCAG 1260 160 GGCCCCTCAC CCTGCCTTAT CTTGCACCCC AAAGCTTTCC TGCCCCAGGC CTGAAAGAGG 1320 161 CTGAGGCCTG GACTTTCCTG CAACTCAAGG ACTTTGNAGC CGGCACAGGG TCTGCTCTTT 1380 162 CTCTGCCAGT GACAGACAGG CTCTTAGCAG CTTCCAGATT GACGACAAGT GCTGAACAGT 1440 163 GGAGGAAGAG GGACAGATGA ATGCCGTGGA TTGCACGTGG NCTCTTGAGC AGTGGCTGGT 1500 164 CCAGGGCTAG TGACTTGGTG TCCCATGATC CCTGTGTTGG TCTCTAGGAG CAGGGATTAA 1560 165 CCTCTGCACT ACTGACAT 1578 167 (2) INFORMATION FOR SEQ ID NO: 3: 169 (i) SEQUENCE CHARACTERISTICS: 170 (A) LENGTH: 639 base pairs 171 (B) TYPE: nucleic acid 172 (C) STRANDEDNESS: single	150	CAGGAAGG	TT T(	JAGG!	EV CALC	י שא	TOUR!	CCCA	CCT	שכטה. ייחייתני	րական TVT	CCTG	I I I GC	IA C	CCCA	AGAGT	
157 GGCTCCTGGT ACTGCTTAG GGTCGCTAAT GCTGTTTCGG TGAAAGGGAT TTATAAACAG 1200 159 ATGCCTGGTT GCTTTAATTT CCTCCGGAAA AAACTTTTCT TTAAAACATC ATAAGGCCAG 1260 160 GGCCCCTCAC CCTGCCTTAT CTTGCACCCC AAAGCTTTCC TGCCCCAGGC CTGAAAGAGG 1320 161 CTGAGGCCTG GACTTTCCTG CAACTCAAGG ACTTTGNAGC CGGCACAGGG TCTGCTCTTT 1380 162 CTCTGCCAGT GACAGACAGG CTCTTAGCAG CTTCCAGATT GACGACAAGT GCTGAACAGT 1440 163 GGAGGAAGAG GGACAGATGA ATGCCGTGGA TTGCACGTGG NCTCTTGAGC AGTGGCTGGT 1500 164 CCAGGGCTAG TGACTTGGTG TCCCATGATC CCTGTGTTGG TCTCTAGGAG CAGGGATTAA 1560 165 CCTCTGCACT ACTGACAT 1578 167 (2) INFORMATION FOR SEQ ID NO: 3: 169 (i) SEQUENCE CHARACTERISTICS: 170 (A) LENGTH: 639 base pairs 171 (B) TYPE: nucleic acid 172 (C) STRANDEDNESS: single																	
159 ATGCCTGGTT GCTTTAATTT CCTCCGGAAA AAACTTTTCT TTAAAACATC ATAAGGCCAG 1260 160 GGCCCCTCAC CCTGCCTTAT CTTGCACCCC AAAGCTTTCC TGCCCCAGGC CTGAAAGAGG 1320 161 CTGAGGCCTG GACTTTCCTG CAACTCAAGG ACTTTGNAGC CGGCACAGGG TCTGCTCTTT 1380 162 CTCTGCCAGT GACAGACAGG CTCTTAGCAG CTTCCAGATT GACGACAAGT GCTGAACAGT 1440 163 GGAGGAAGAG GGACAGATGA ATGCCGTGGA TTGCACGTGG NCTCTTGAGC AGTGGCTGGT 1500 164 CCAGGGCTAG TGACTTGGTG TCCCATGATC CCTGTGTTGG TCTCTAGGAG CAGGGATTAA 1560 165 CCTCTGCACT ACTGACAT 1578 167 (2) INFORMATION FOR SEQ ID NO: 3: 169 (i) SEQUENCE CHARACTERISTICS: 170 (A) LENGTH: 639 base pairs 171 (B) TYPE: nucleic acid 172 (C) STRANDEDNESS: single																	
160 GGCCCCTCAC CCTGCCTTAT CTTGCACCCC AAAGCTTTCC TGCCCCAGGC CTGAAAGAGG 1320 161 CTGAGGCCTG GACTTTCCTG CAACTCAAGG ACTTTGNAGC CGGCACAGGG TCTGCTCTTT 1380 162 CTCTGCCAGT GACAGACAGG CTCTTAGCAG CTTCCAGATT GACGACAAGT GCTGAACAGT 1440 163 GGAGGAAGAG GGACAGATGA ATGCCGTGGA TTGCACGTGG NCTCTTGAGC AGTGGCTGGT 1500 164 CCAGGGCTAG TGACTTGGTG TCCCATGATC CCTGTGTTGG TCTCTAGGAG CAGGGATTAA 1560 165 CCTCTGCACT ACTGACAT 1578 167 (2) INFORMATION FOR SEQ ID NO: 3: 169 (i) SEQUENCE CHARACTERISTICS: 170 (A) LENGTH: 639 base pairs 171 (B) TYPE: nucleic acid 172 (C) STRANDEDNESS: single																	
161 CTGAGGCCTG GACTTTCCTG CAACTCAAGG ACTTTGNAGC CGGCACAGGG TCTGCTCTTT 1380 162 CTCTGCCAGT GACAGACAGG CTCTTAGCAG CTTCCAGATT GACGACAAGT GCTGAACAGT 1440 163 GGAGGAAGAG GGACAGATGA ATGCCGTGGA TTGCACGTGG NCTCTTGAGC AGTGGCTGGT 1500 164 CCAGGGCTAG TGACTTGGTG TCCCATGATC CCTGTGTTGG TCTCTAGGAG CAGGGATTAA 1560 165 CCTCTGCACT ACTGACAT 1578 167 (2) INFORMATION FOR SEQ ID NO: 3: 169 (i) SEQUENCE CHARACTERISTICS: 170 (A) LENGTH: 639 base pairs 171 (B) TYPE: nucleic acid 172 (C) STRANDEDNESS: single	159	CCCCCCTC	אר כי	CT111	הלטוט או באבד די	י כיים. יי	TGCA	CCCC	ΔΔΔ	ጋርጥጥ፣ ገርጥጥ፣	TCC	ፐርሮር	TCAGO	G C	ТСАА	AGAGG	
162 CTCTGCCAGT GACAGACAGG CTCTTAGCAG CTTCCAGATT GACGACAAGT GCTGAACAGT 163 GGAGGAAGAG GGACAGATGA ATGCCGTGGA TTGCACGTGG NCTCTTGAGC AGTGGCTGGT 164 CCAGGGCTAG TGACTTGGTG TCCCATGATC CCTGTGTTGG TCTCTAGGAG CAGGGATTAA 165 CCTCTGCACT ACTGACAT 167 (2) INFORMATION FOR SEQ ID NO: 3: 169 (i) SEQUENCE CHARACTERISTICS: 170 (A) LENGTH: 639 base pairs 171 (B) TYPE: nucleic acid 172 (C) STRANDEDNESS: single																	
163 GGAGGAAGAG GGACAGATGA ATGCCGTGGA TTGCACGTGG NCTCTTGAGC AGTGGCTGGT 1500 164 CCAGGGCTAG TGACTTGGTG TCCCATGATC CCTGTGTTGG TCTCTAGGAG CAGGGATTAA 1560 165 CCTCTGCACT ACTGACAT 1578 167 (2) INFORMATION FOR SEQ ID NO: 3: 169 (i) SEQUENCE CHARACTERISTICS: 170 (A) LENGTH: 639 base pairs 171 (B) TYPE: nucleic acid 172 (C) STRANDEDNESS: single	162	CTGAGGCC	16 G	ACAC:	ACAC(	3 CM	~mm∆ı	CCAG	CTT	CAG	יייים	GACG	ACAA	T G	CTGA	ACAGT	
164 CCAGGGCTAG TGACTTGGTG TCCCATGATC CCTGTGTTGG TCTCTAGGAG CAGGGATTAA 1560 165 CCTCTGCACT ACTGACAT 1578 167 (2) INFORMATION FOR SEQ ID NO: 3: 169 (i) SEQUENCE CHARACTERISTICS: 170 (A) LENGTH: 639 base pairs 171 (B) TYPE: nucleic acid 172 (C) STRANDEDNESS: single	162	CCACCAAG	AC C	CACA	CATC	Δ ΤΥ Δ ΤΥ Δ	3006	TGGA	TTG	CACG	TGG	NCTC'	TTGAC	GC A	GTGG	CTGGT	
167 CCTCTGCACT ACTGACAT  167 (2) INFORMATION FOR SEQ ID NO: 3:  169 (i) SEQUENCE CHARACTERISTICS:  170 (A) LENGTH: 639 base pairs  171 (B) TYPE: nucleic acid  172 (C) STRANDEDNESS: single	164	CCACCCCT	ልር ጥ	こみでか	ፓርርጥ(	. TIL	CCATI	CATC	ССТО	GTGT'	TGG	тстс'	TAGG	AG C	AGGG	ATTAA	
167 (2) INFORMATION FOR SEQ ID NO: 3: 169 (i) SEQUENCE CHARACTERISTICS: 170 (A) LENGTH: 639 base pairs 171 (B) TYPE: nucleic acid 172 (C) STRANDEDNESS: single						, 10	CCITI	02110	001	0101							
169 (i) SEQUENCE CHARACTERISTICS: 170 (A) LENGTH: 639 base pairs 171 (B) TYPE: nucleic acid 172 (C) STRANDEDNESS: single	105 CCICIOCHCI MOIOMA																
170 (A) LENGTH: 639 base pairs 171 (B) TYPE: nucleic acid 172 (C) STRANDEDNESS: single																	
171 (B) TYPE: nucleic acid 172 (C) STRANDEDNESS: single																	
172 (C) STRANDEDNESS: single	· · ·																
· ·																	

60

DATE: 12/07/2001 RAW SEQUENCE LISTING PATENT APPLICATION: US/09/961,201 TIME: 12:18:53

Input Set : N:\Crf3\RULE60\09961201.txt Output Set: N:\CRF3\12072001\I961201.raw

```
(ii) MOLECULE TYPE: cDNA
175
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
177
179 CTGACTGCCA AGAAAATGGT GCTGGCTTTG CTGGAGCTGG CGCGGCAGGA CCACGGTGCT
180 CTGGACTGCT GCGTGGTGGT CATTCTCTCT CACGGCTGTC AGGCCAGCCA CCTGCAGTTC
                                                                          120
181 CCAGGGGCTG TCTACGGCAC AGATGGATGC CCTGTGTCGG TCGAAAAGAT TGTGAACATC
                                                                          180
182 TTCAATGGGA CCAGCTGCCC CAGCCTGGGA GGGAAGCCCA AGCTCTTTTT CATCCAGGCC
183 TGTGGTGGGG AGCAGAAGA CCATGGGTTT GAGGTGGCCT CCACTTCCCC TGAAGACGAG
184 TCCCCTGGCA GTAACCCCGA GCCAGATGCC ACCCCGTTCC AGGAAGGTTT GAGGACCTTC
185 GACCAGCTGG ACGCCATATC TAGTTTGCCC ACACCCAGTG ACATCTTTGT GTCCTACTCT
                                                                          420
186 ACTTTCCCAG GTTTTGTTTC CTGGAGGGAC CCCAAGAGTG GCTCCTGGTA CGTTGAGACC
187 CTGGACGACA TCTTTGAGCA GTGGGCTCAC TCTGAAGACC TGCAGTCCCT CCTGCTTAGG
                                                                          540
188 GTCGCTAATG CTGTTTCGGT GAAAGGGATT TATAAACAGA TGCCTGGTTG CTTTAATTTC
                                                                          600
189 CTCCGGAAAA AACTTTTCTT TTAAAACATC ATAAGGCAG
                                                                          639
191 (2) INFORMATION FOR SEQ ID NO: 4:
193
         (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 203 amino acids
194
195
              (B) TYPE: amino acid
196
              (C) STRANDEDNESS: single
197
              (D) TOPOLOGY: linear
        (ii) MOLECULE TYPE: protein
199
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
201
     Met Val Leu Ala Leu Leu Glu Leu Ala Arg Gln Asp His Gly Ala Leu
203
204
                                          10
205
     Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln Ala Ser His
206
                                      25
                 20
     Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys Pro Val Ser
207
208
                                 40
     Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys Pro Ser Leu
209
                             55
210
     Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly Gly Glu Gln
211
                         70
                                              75
212
     Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu Asp Glu Ser
213
214
                                          90
215
     Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln Glu Gly Leu
                                      105
                                                          110
216
                 100
217
     Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro Thr Pro Ser
                                 120
218
     Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val Ser Trp Arg
219
                                                  140
220
                             135
     Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp Asp Ile Phe
221
222
                         150
                                              155
     Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu Leu Arg Val
223
                                                              175
224
                     165
                                          170
     Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met Pro Gly Cys
225
226
     Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Met
227
228
             195
230 (2) INFORMATION FOR SEQ ID NO: 5:
         (i) SEQUENCE CHARACTERISTICS:
```



DATE: 12/07/2001

TIME: 12:18:53

Input Set : N:\Crf3\RULE60\09961201.txt
Output Set: N:\CRF3\12072001\1961201.raw

PATENT APPLICATION: US/09/961,201

RAW SEQUENCE LISTING

```
233
               (A) LENGTH: 34 base pairs
234
               (B) TYPE: nucleic acid
235
               (C) STRANDEDNESS: single
236
               (D) TOPOLOGY: linear
238
        (ii) MOLECULE TYPE: cDNA
240
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
242 GAACGGGTA CCGCCATGGA CGAAGCGGAT CGGC
                                                                           34
244 (2) INFORMATION FOR SEQ ID NO: 6:
246
         (i) SEQUENCE CHARACTERISTICS:
247
               (A) LENGTH: 60 base pairs
248
               (B) TYPE: nucleic acid
249
               (C) STRANDEDNESS: single
250
              (D) TOPOLOGY: linear
252
        (ii) MOLECULE TYPE: cDNA
254
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
256 TGCTCTAGAT TAGTGGTGGT GGTGGTGGTG TGATGTTTTA AAGAAAAGTT TTTTCCGGAG
                                                                            60
258 (2) INFORMATION FOR SEQ ID NO: 7:
260
         (i) SEQUENCE CHARACTERISTICS:
261
              (A) LENGTH: 41 base pairs
262
              (B) TYPE: nucleic acid
263
              (C) STRANDEDNESS: single
264
              (D) TOPOLOGY: linear
266
        (ii) MOLECULE TYPE: cDNA
268
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
270 AAGCTCTTTT TCATCCAGGC CGCGGGTGGG GAGCAGAAGA C
                                                                            41
272 (2) INFORMATION FOR SEQ ID NO: 8:
274
        (i) SEQUENCE CHARACTERISTICS:
275
              (A) LENGTH: 39 base pairs
276
              (B) TYPE: nucleic acid
277
              (C) STRANDEDNESS: single
278
              (D) TOPOLOGY: linear
280
        (ii) MOLECULE TYPE: cDNA
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
282
284 GTCTTTCTGC TCCCCACCCG CGGCCTGGAT GAAAAAAGC
                                                                            39
286 (2) INFORMATION FOR SEQ ID NO: 9:
288
        (i) SEQUENCE CHARACTERISTICS:
289
              (A) LENGTH: 66 base pairs
290
              (B) TYPE: nucleic acid
291
              (C) STRANDEDNESS: single
292
              (D) TOPOLOGY: linear
        (ii) MOLECULE TYPE: cDNA
294
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
296
298 TGCTCTAGAT TACTTGTCAT CGTCGTCCTT GTAGTCTGAT GTTTTAAAGT TAAGTTTTTT
                                                                           60
299 CCGGAG
                                                                           66
301 (2) INFORMATION FOR SEQ ID NO: 10:
         (i) SEQUENCE CHARACTERISTICS:
304
              (A) LENGTH: 5 amino acids
305
              (B) TYPE: amino acid
306
              (C) STRANDEDNESS: single
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VERIFICATION SUMMARY

DATE: 12/07/2001 PATENT APPLICATION: US/09/961,201 TIME: 12:18:54

Input Set : N:\Crf3\RULE60\09961201.txt Output Set: N:\CRF3\12072001\I961201.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]